

TITLE \_\_\_\_\_

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Sent 8 samples back to microchemistry to read from other end. - Mφ #s 902, 904, 905, 911, 912, 913, 917, 918

### DNA SEQUENCING REQUEST

Microchemistry Department

Requested by Heather Pearson Date \_\_\_\_\_  
 Notebook Reference(s): 95-1065 p. 13 Project: 16  
 Vector: PRC CMV Host: X4 # of Clones 8  
 (Please indicate size)  
 Names of Sample(s): Mφ 902, 904, 905, 908, 911, 912, 917, 918  
 (Please provide OD<sub>260</sub> and insert size)  
 Sequencing Primer(s): OC03  
 (Note: sequencing primers should be at 5μg/ml)

## Check one

- ☐ Long run (-14 hrs/-550bp)  
☒ Short run (-7hrs/-500bp) Data can be provided the same day samples are run

## Check one

- ☒ DS-DNA template (we need 1μg/μsu. or primer)  
☐ SS-DNA template (we need 500μg/μsu. or primer)  
☐ PCR fragment (amt. we need depends on size and purity)  
☐ Phage lysate

All templates will be sequenced with Taq-Dye Terminator Chemistry.

Other Instructions:

Mφ 902 MC 17701 HS. cDNA clone 1  
 Mφ 904 MC 17702 HS. cDNA clone 5/2nd SE  
 Mφ 908 MC 17704 HS. cDNA clone 112  
 911 MC 17705 hum. cytochrome mRNA  
 912 MC 17706 Rat nov. sprague dawley col.  
 913 MC 17703 Bovine microsatellite  
 917 MC 17707 Bact Sequence

100% (65/65) T90395  
 96% (246/255) T32201  
 98% (207/210) T85702  
 63% (57/245) M80922  
 62% (106/170) U0836  
 68% (42/61) L37252

959 MC 17705 HS. cDNA clone 78114 3' 98% (12/12) T61622

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Witnessed &amp; Understood by me,

Date

Invented by

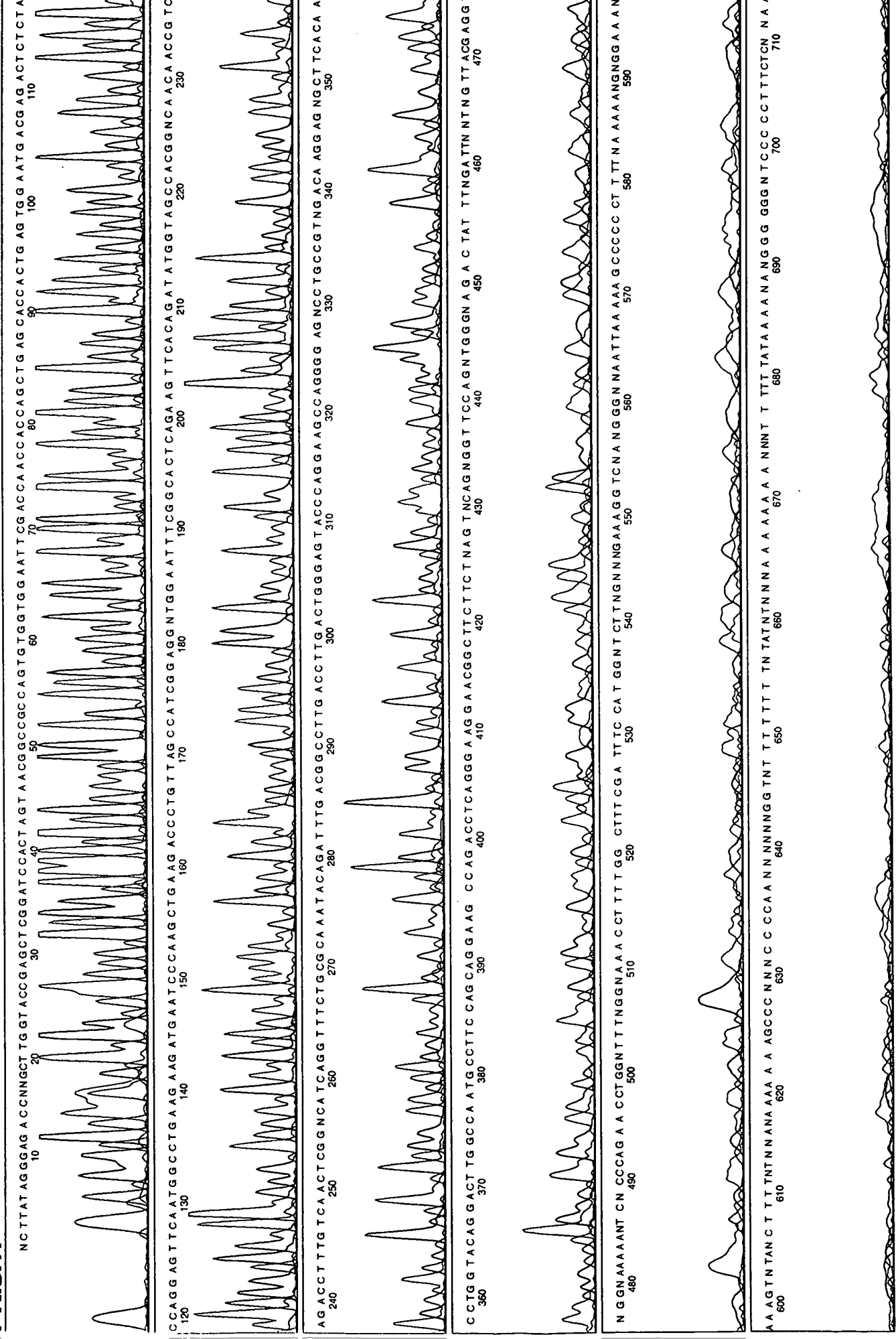
Date

Pant H Steiner

Recorded by

Heather Pearson

Spacing: 11.63 Adaptive



**cc:Mail for: heather.pearson**

**Subject: Re: 17705**

**From:** "NCBI BLAST E-Mail Server" <blast@ncbi.nlm.nih.gov>

**To:** Heather Pearson

gb	M80927	HUMHA3G	Human glycoprotein mRNA, complete cds.	427	6.2e-26	1
gb	U19900	SSU19900	Sus scrofa 38kDa heparin-binding gly...	358	4.6e-20	1
gb	U02270	MSU02270	Manduca sexta chitinase mRNA, comple...	308	8.2e-16	1
gb	M57601	BACCHIA3	B.circulans chitinase A1 (chiA) gene...	223	1.2e-08	1
gb	L14614	TRRENDOCHI	Trichoderma harzianum endochitinase ...	173	0.00020	1
emb	X79381	THECH42	T.harzianum (IMI 206040) ech-42 gene.	173	0.00020	1
emb	X64104	AACH11A	A.album chil gene for chitinase	130	0.56	1
gb	U13646	CELZK783	Caenorhabditis elegans cosmid ZK783.	129	0.65	1
dbj	D12647	STMCHIC	S.lividans gene for chitinase C, com...	124	0.93	1
gb	M82804	STMCHTA	Streptomyces plicatus chitinase 63 (...)	124	0.93	1
gb	T92100	T92100	ye01h11.r1 Homo sapiens cDNA clone 1...	123	0.94	1
emb	X15208	SMCHIB	Serratia marcescens chiB gene for ch...	119	0.9991	1
emb	Z36295	SHCHITB	S.marcescens (BJL200) chiB gene for ...	119	0.9991	1

>gb|M80927|HUMHA3G Human glycoprotein mRNA, complete cds.

Length = 1741

Plus Strand HSPs:

Score = 427 (118.0 bits), Expect = 6.2e-26, P = 6.2e-26

Identities = 157/248 (63%), Positives = 157/248 (63%), Strand = Plus / Plus

Query: 2 ACCAACCACCAGCTGAGCACCCTGAGTGGAATGACGAGACTCTCTACCAGGAGTTCAT 61

Sbjct: 255 AGCAACGATCACATCGACACCTGGGAGTGGGAATGATGTGACGCTCTACGGCATGCTCAAC 314

Query: 62 GGCCTGAAGAAGATGAATCCCAAGCTGAAGACCTGTTAGCCATCGGAGGNTGGAATTTC 121

Spict: 315 A C A C T C A A G A A C A G G A A C C C C A A C C T G A A G A C T C T C T G T G T C T G T C G G A G G A T G G A A C T T T 374

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>gb|U19900|SSU19900 Sus scrofa 38kDa heparin-binding glycoprotein mRNA,  
complete cds. >emb|Z47803|SSGP38KD S.scrofa 38kDa heparin-binding  
glycoprotein.
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Length = 1733

Plus Strand HSPs:

Score = 358 (98.9 bits), Expect = 4.6e-20, P = 4.6e-20

Identities = 148/245 (60%), Positives = 148/245 (60%), Strand = Plus / Plus

Query: 2 ACCAACCACCAGCTGAGCACCCTGAGTGGAAATGACGAGACTCTCTACCAGGAGTTCAAT 61

Sbjct: 250 AGCAACAATGAGATTGACACCTTGGAGTGGAAATGATGTGACGCTCTATGACACACTGAAC 309

Query: 62 GGCCTGAAGAAGATGAATCCCAAGCTGAAGACCCTGTTAGCCATCGGAGGNTGGAATTTT 121

Sbjct: 310 ACACTCAAGAACAGGAACCCCAACCTGAAGACCCCTCTGTCTGTGTGGAGGATGGAACCTTT 369

>gb|U02270|MSU02270 Manduca sexta chitinase mRNA, complete cds.

Length = 2452

Plus Strand HSPs:

Score = 308 (85.1 bits), Expect = 8.2e-16, P = 8.2e-16

Identities = 110/172 (63%), Positives = 110/172 (63%), Strand = Plus / Plus

Query: 76 GAATCCCAAGCTGAAGACCCTGTTAGCCATCGGAGGNTGGAATTTTCGGCACTCAGAAGTT 135

Sbjct: 309 GCATCCCAGCGTCAAGTTTCATGGTAGCGGTGGGCGGCTGGGCTGAAGGCAGTTTCGAAGTA 368